

AMENDMENTS

Listing of claims:

This listing of claims will replace all prior versions, and listings, of claims in the application.

1. **(Original)** A method executed by a computer under the control of a program, said computer including a memory for storing said program, said method comprising the steps of:
 - (A) receiving a protein backbone structure with variable residue positions;
 - (B) establishing a group of potential rotamers for each of said variable residue positions, wherein at least one variable residue position has rotamers from at least two different amino acid side chains; and
 - (C) analyzing the interaction of each of said rotamers with all or part of the remainder of said protein structure to generate a set of optimized protein sequences, where said analyzing step includes a Hybrid Exact Rotamer Optimization (HERO) step.
2. **(Original)** A method according to claims 1 wherein said set of optimized protein sequences comprises the globally optimal protein sequence.
3. **(Original)** A method according claims 1 wherein said analyzing step includes the use of at least one scoring function.
4. **(Original)** A method according to claim 3 wherein said scoring function is selected from the group consisting of van der Waals potential scoring function, a hydrogen bond potential scoring function, an atomic solvation scoring function, an electrostatic scoring function, and a secondary structure propensity scoring function.
5. **(Original)** A method according to claim 3 wherein said analyzing step includes the use of at least two scoring functions.
6. **(Original)** A method according to claim 3 wherein said analyzing step includes the use of at least three scoring functions.
7. **(Original)** A method according to claim 3 wherein said analyzing step includes the use of at least four scoring functions.
8. **(Original)** A method according to claim 3 wherein said atomic solvation scoring function includes a scaling factor that compensates for over-counting.
9. **(Original)** A method according to claims 1 further comprising testing at least one member of said set to produce experimental results.
10. **(Original)** A method according to claim 2 further comprising:
 - (D) generating a rank ordered list of additional optimal sequences from said global optimal protein sequence.

11. **(Original)** A method according to claim 10 wherein said generating includes the use of a Monte Carlo search.
12. **(Original)** A method according to claim 1 wherein said analyzing step comprises a Monte Carlo computation.
13. **(Original)** A method according to claim 10 further comprising:
(E) testing some or all of said protein sequences from said ordered list to produce potential energy test results.
14. **(Original)** A method according to claim 13 further comprising:
(F) analyzing the correspondence between said potential energy test results and theoretical potential energy data.
15. **(Original)** A method according to claim 1 further comprising altering at least one supersecondary structure parameter value of said protein backbone structure prior to establishing said potential rotamer group.
16. **(Cancelled)**
17. **(Cancelled)**
18. **(Cancelled)**
19. **(Cancelled)**
20. **(Original)** A computer readable memory to direct a computer to function in a specified manner, comprising:
a side chain module to correlate a group of potential rotamers for residue positions of a protein backbone model;
a ranking module to analyze the interaction of each of said rotamers with all or part of the remainder of said protein to generate a set of optimized protein sequences wherein said analysis includes a HERO computation step.
21. **(Original)** A computer readable memory according to claim 20 wherein said ranking module includes a van der Waals scoring function component.
22. **(Original)** A computer readable memory according to claim 20 wherein said ranking module includes an atomic solvation scoring function component.
23. **(Original)** A computer readable memory according to claim 20 wherein said ranking module includes a hydrogen bond scoring function component.
24. **(Original)** A computer readable memory according to claim 20 wherein said ranking module includes a secondary structure scoring function component.
25. **(Original)** A computer readable memory according to claim 20 further comprising

an assessment module to assess the correspondence between potential energy test results and theoretical potential energy data.

27. (New) A method according to claim 1 further comprising making at least one protein from said set of protein optimized protein sequences.

28. (New) A method according to claim 27 further comprising testing said protein to produce experimental results wherein said results comprise testing for stability and function.